

# AN INTRODUCTION TO SPECTRAL DISTANCES IN NETWORKS (EXTENDED VERSION)

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**ABSTRACT.** Many functions have been recently defined to assess the similarity among networks as tools for quantitative comparison. They stem from very different frameworks - and they are tuned for dealing with different situations. Here we show an overview of the spectral distances, highlighting their behavior in some basic cases of static and dynamic synthetic and real networks.

## INTRODUCTION

Citing a comprehensive review [1], a complex network is a graph whose structure is irregular and dynamically evolving in time. In terms of architectures, Strogatz [2] used the term "complex" to describe a network that is the counterpart of "regular" graphs (chains, grids, lattices and fully-connected graphs), the random graphs lying at the extremal edge of the complexity spectrum. Network models from empirical studies lie somewhere in between regularity and randomness; although more often unbalanced towards the latter, they can have to unexpectedly highly symmetric structures [3].

This article reviews and benchmarks a class of methods that tackle the problem of comparing structure between networks. Structure and structural properties of networks have been studied in a wide variety of fields in science [4, 5, 6, 1], with methods ranging from statistical physics to machine learning [7, 8]. Structural analysis is of central importance in computational biology [9]. Coates pointed out that the comparison of biological networks can provide much more evolutionary information than studying each network separately [10]. Furthermore, the comparison of protein interaction networks can help designing models of cellular functions [11, 12]. Comparison methods are essential with dynamic networks to measure differences between two consecutive network states and then model the whole series. Comparison is also essential in network reconstruction (e.g. of gene regulation networks) by structure reverse engineering starting from steady-state or time series data [13, 14, 15], where performance has to be gauged against the ground truth of a real or simulated network.

Our interest for network comparison is motivated by the study of network stability. On this less beaten path, only network robustness with respect to perturbations has been considered until now [16, 17]. It is envisioned that the choice of appropriate measures between networks would enable new model selection procedures such those available in molecular profiling for sets of ranked gene lists [18].

In this study, six candidate distances derived from the family of spectral similarity measures are investigated for network comparison. After a first presentation of spectral measures and alternatives in the rest of this introduction, a technical overview is provided in Sect. 2 and candidate measures are presented. Benchmark data and experiments devised to exemplify and compare the candidates are presented in Sect. 3.

**Related Work.** The basic goal of network comparison is quantifying difference between two homogeneous objects in some network space. The theory of network measurements relies on the quantitative description of main properties such as degree distribution and correlation, path lengths, diameter, clustering, presence of motives [19]. These and other properties have been described for complex networks in [5, 1] and recently reviewed by MacArthur and Sánchez-García [20]. Furthermore, network measurements can be encoded into a feature vector, yielding a representation convenient for classification tasks [21].

The use of similarity measures on the topology of the underlying graphs defines a different strategy, whose roots date back to the 70's with the theory of graph distances (regarding both metrics inter- and intra-graphs [22]). Since then, a number of similarity measures have been introduced, including metrics relaxed to less stringent bounds. Cost-based functions stems from the parallel theory of graph alignment: the edit distance and its variants use the minimum cost of transformation of one graph into another by means of the usual edit operations - insertion and deletion of links.

Feature-based measures are instead obtained when the similarity function is based on measurements feature vectors. One notable example in this family is the recently proposed use of  $\zeta$ -functions for network volume measurements [23, 24].

Finally, the label “structure-based” distance groups all other measures that do not rely on cost functions or characteristic features. A typical example are those measures based on functions of the maximal common subgraphs between the two networks, or those based on the common motifs [25], i.e. patterns of interconnections occurring in complex networks significantly more often than in randomized networks. Remarkably, equivalence of some structure-based distance and the edit distance has been proven [26]). Although in most cases only network topology is considered, measures were also introduced that deal with directed or weighted links: for an example of a generic construction and an application to biological networks, see [27].

The family of spectral measures, which is investigated in this paper, is also part of the group of structure-based distances. Basically, it consists of a variety of maps of network's eigenvalues. The theory of graph spectra started in the early 50's and since then many of its aspects have been deeply mined, including a first classification of networks [28]. The spectral theory has been applied to biological networks [29, 30], where the properties of being scale-free (the degree distribution following a power law) and small-world (most nodes are not neighbors of one another, but most nodes can be reached from every other by a small number of hops or steps) are particularly evident. Estimates (also asymptotic) of the eigenvalues distribution are available for complex networks [31]. The idea of using spectral measures for network comparison is instead only recent and it relies on similarity measures that are functions of the network eigenvalues. However, it is important to note that, because of the existence of isospectral networks, all these measures are indeed distances between classes of isospectral graphs. An overview of the most common spectral similarity measures and of their basic properties is presented in the rest of this paper.

## 1. NOTATIONS

Formally, any network can be represented as a graph, a mathematical entity consisting of  $N$  nodes (vertices) and  $E$  edges (links or arrows) connecting pairs of nodes and representing interactions ( $N \in \mathbb{N} \cup \{\infty\}$ ). Loops are allowed, i.e. an edge can link the same node to indicate self-interaction (some authors use the term pseudograph to indicate graph with loops). Edges can be bidirectional or unidirectional: in the latter case the graph is called directed (digraph, for short) and the edges are represented by arrows. Moreover,

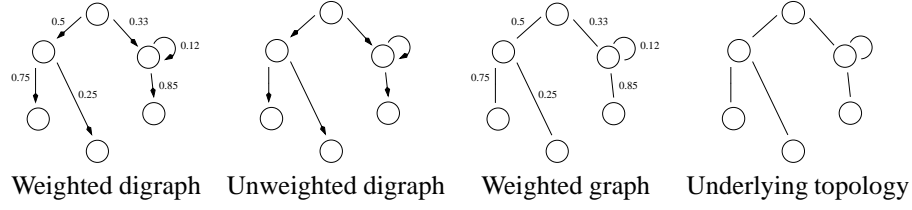
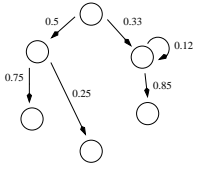
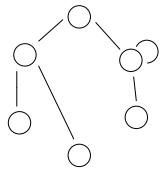


FIGURE 1. Network types

edges can carry weights to indicate interaction intensity: in this case, the network is called weighted. More refined structures exist but they are not considered here. For instance: labeled graphs, where functions from some subsets of the integers to the vertices (edges) of the graph identify classes of vertices (edges); hypergraphs, where an edge can connect any number of vertices; and multigraphs, where any numbers of edges between two vertices are allowed. For any network  $G$ , its topology consists of the set  $V(G) = \{v_1, \dots, v_N\}$  of its nodes and the set  $E(G) = \{e_1 = (v_{i_1}, v_{j_1}), \dots, e_E = (v_{i_E}, v_{j_E})\}$  of its edges, neglecting weights and directions. Different types of graph sharing the same topology are displayed in Fig. 1.

A network, or graph, is characterized completely by its adjacency matrix  $A$ , i.e. an  $N \times N$  matrix whose nonzero entries denote the various links between the graph's  $N$  nodes. Directions and weights are represented by the signs (or by asymmetry) and values of the matrix entries. For the underlying topology (and thus for any unweighted undirected network), the adjacency matrix is symmetric and with entries in  $\{0, 1\}$ . The adjacency matrices for the weighted digraph in Fig. 1 and its topology are shown in Tab. 1, where nodes ordering is clockwise starting from the top node. This representation is not unique, in that it depends on the actual labeling of the nodes, and isomorphic graphs (identical graphs with permuted labels) share the same adjacency matrix. Similarly, graphical representations are not unique too, since node placement is arbitrary.

TABLE 1. Adjacency matrices for the weighted directed network (two alternative matrices, with sign indicating direction or asymmetric, with the (positive) value only in entry  $(i, j)$  if  $i \rightarrow j$ ) in Fig. 1 and its topology; nodes ordering is clockwise starting from the top node.

Network	Adjacency matrix
	$\begin{pmatrix} 0 & 0.33 & 0 & 0 & 0 & 0.5 \\ (-0.33) & 0.12 & 0.85 & 0 & 0 & 0 \\ 0 & (-0.85) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & (-0.25) \\ 0 & 0 & 0 & 0 & 0 & (-0.75) \\ (-0.5) & 0 & 0 & 0.25 & 0.75 & 0 \end{pmatrix}$
	$\begin{pmatrix} 0 & 1 & 0 & 0 & 0 & 1 \\ 1 & 1 & 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 1 & 1 & 0 \end{pmatrix}$

The degree ( $\deg$ ) of a vertex in an undirected graph is the number of edges touching the vertex itself, with loops (usually, but not for all authors) counted twice. The degree matrix is the diagonal matrix with the vertex degrees: for instance, for the network topology in Fig. 1, the degree matrix is  $D = \begin{pmatrix} 2 & & & \\ & 4 & & \\ & & 1 & \\ & & & 1 & \\ & & & & 1 & \\ & & & & & 3 \end{pmatrix}$ . The Laplacian matrix of a graph is defined as the difference between the degree and the adjacency matrices:  $L = D - A$ . Thus, for an undirected and unweighted graph with no loops (a simple graphs),  $L$  has zero row/column sum.

There exist at least two different normalized versions of the Laplacian matrix, namely  $\mathcal{L} = D^{-\frac{1}{2}} L D^{-\frac{1}{2}} = I - D^{-\frac{1}{2}} A D^{-\frac{1}{2}}$  and  $\Delta = D^{\frac{1}{2}} \mathcal{L} D^{-\frac{1}{2}}$ , where  $I$  is the identity matrix and  $D^{-\frac{1}{2}}$  is the diagonal matrix with entries  $-\frac{\delta_{ij}}{\sqrt{\deg_i}}$ . In terms of the degree, their entries can be explicitly written as:

$$\mathcal{L} = \begin{cases} 1 & \text{if } i = j \text{ and } \deg_i \neq 0 \\ -\frac{1}{\sqrt{\deg_i \deg_j}} & \text{if } ij \text{ is an edge} \\ 0 & \text{otherwise} \end{cases} \quad \Delta = \begin{cases} 1 & \text{if } i = j \text{ and } \deg_i \neq 0 \\ -\frac{1}{\deg_j} & \text{if } ij \text{ is an edge} \\ 0 & \text{otherwise} \end{cases}$$

The matrices  $\mathcal{L}$  and  $\Delta$  are similar so they have the same set of eigenvalues (spectrum).

The matrices  $A, L, \mathcal{L}$  and  $\Delta$  are called connectivity matrices of the graph. An approach to connectivity matrices also in terms of the normalized Laplacian operators can be found in [32, 33, 34].

An undirected and unweighted graph has symmetric real connectivity matrices and therefore real eigenvalues and a complete set of orthonormal eigenvectors. Also, for each eigenvalue, its algebraic multiplicity coincides with its geometric multiplicity. Since  $A$  has zero diagonal, its trace and hence the sum of the eigenvalues is zero. Moreover,  $L$  is positive semidefinite and singular, so the eigenvalues are  $0 = \mu_0 \leq \mu_1 \leq \dots \leq \mu_{n-1}$  and their sum (the trace of  $L$ ) is twice the number of edges. Finally, the eigenvalues of  $\mathcal{L}$  lie in the range  $[0, 2]$ .

While the connectivity matrices depend on the vertex labeling, the spectrum is a graph invariant. Two graphs are called isospectral or cospectral if the corresponding connectivity matrices of the graphs have equal multisets of eigenvalues. Isospectral graphs need not be isomorphic, but isomorphic graphs are always isospectral. Network classification in terms of their spectrum is still an open problem [35, 36, 37]: however, a first attempt to (qualitative) network classification in terms of graph spectra can be found in [28, 38] by Banerjee.

For an introduction to the theory of graph spectra, see [39, 40, 41]. The relation between the spectral properties of the connectivity matrices and the structure and the dynamics of the networks are discussed in [42, 32, 43].

## 2. OVERVIEW OF SPECTRAL SIMILARITY MEASURES

In this section, we introduce a set of similarity measures based on the graph spectra that was recently proposed in literature, following an ideal chronological timeline.

The first distance D1 (or, indeed, one-parameter family of distances) we are presenting is possibly the most natural one. Originally D1 was introduced as an intra-graph measure [44, 45] and mentioned as an inter-graph distance by Pincombe [46], for evaluating changes in time-series of graphs. Let  $G, H$  be two graphs with  $N$  nodes and let  $\{\lambda_0 = 0 \leq \lambda_1 \leq \dots \leq \lambda_{N-1}\}, \{\mu = 0 \leq \mu \leq \dots \leq \mu_{N-1}\}$  the respective Laplacian spectra. For an

integer  $k \leq N$ , the distance is defined as:

$$(1) \quad d_k(G, H) = \begin{cases} \sqrt{\frac{\sum_{i=N-k}^{N-1} (\lambda_i - \mu_i)^2}{\sum_{i=N-k}^{N-1} \lambda_i^2}} & \text{if } \sum_{i=N-k}^{N-1} \lambda_i^2 \leq \sum_{i=N-k}^{N-1} \mu_i^2 \\ \sqrt{\frac{\sum_{i=N-k}^{N-1} (\lambda_i - \mu_i)^2}{\sum_{i=N-k}^{N-1} \mu_i^2}} & \text{if } \sum_{i=N-k}^{N-1} \mu_i^2 < \sum_{i=N-k}^{N-1} \lambda_i^2 \end{cases}$$

The D1 measure is non-negative, separated, symmetric and it satisfies the triangle inequality, so it is a measure.

A more refined spectral distance was defined as a step towards reconstructing a graph from its spectrum through a Metropolis algorithm [47]. The definition of the measure D2 follows the dynamical interpretation of a  $N$ -nodes network as a  $N$ -atoms molecules connected by identical elastic strings, where the pattern of connections is defined by the adjacency matrix of the corresponding network. The dynamical system is described by the set of  $N$  differential equations

$$\ddot{x}_i + \sum_{j=1}^N A_{ij}(x_i - x_j) = 0 \quad \text{for } i = 0, \dots, N-1.$$

The vibrational frequencies  $\omega_i$  are given by the eigenvalues of the Laplacian matrix<sup>1</sup> of the network:  $\lambda_i = \omega_i^2$ , with  $\lambda_0 = \omega_0 = 0$ . The spectral density for a graph as the sum of Lorentz distributions is defined as

$$\rho(\omega) = K \sum_{i=1}^{N-1} \frac{\gamma}{(\omega - \omega_k)^2 + \gamma^2}$$

where  $\gamma$  is the common width<sup>2</sup> and  $K$  is the normalization constant solution of

$$\int_0^\infty \rho(\omega) d\omega = 1.$$

Then the spectral distance  $\epsilon$  between two graphs  $G$  and  $H$  with densities  $\rho_G(\omega)$  and  $\rho_H(\omega)$  can then be defined as

$$(2) \quad \epsilon(G, H) = \sqrt{\int_0^\infty [\rho_G(\omega) - \rho_H(\omega)]^2 d\omega}.$$

Note that two above integrals can be explicitly computed through the relation  $\int \frac{1}{1+x^2} dx = \arctan(x)$ .

A simpler measure D3 was introduced in [48] for graph matching, using the graph edit distance as the reference baseline. The authors compute the spectrum associated to the

<sup>1</sup>In [39], the Laplacian spectrum is called the vibrational spectrum.

<sup>2</sup>The scale parameter  $\gamma$  which specifies the half-width at half-maximum (HWHM), equal to half the interquartile range.

classical adjacency matrix, Laplacian matrix, signless Laplacian matrix  $|L| = D + A$ , and normalized Laplacian ( $\mathcal{L}$ ) matrix. They also introduce two more functions: the path length distribution and the heat kernel  $h_t$ . The heat kernel is related to the Laplacian by the equation

$$\frac{\partial h_t}{\partial t} = -Lh_t ,$$

so that

$$h_t(u, v) = \sum_{i=0}^{N-1} e^{-\lambda_i t} \phi_i(u) \phi_i(v) ,$$

where  $\lambda_i$  are the Laplacian eigenvalues and  $\phi_i$  the corresponding eigenvectors. For  $t \rightarrow 0$ ,  $h_t \rightarrow I - Lt$ , while when  $t \rightarrow \infty$  then  $h_t \rightarrow e^{-\lambda_{N-1} t} \phi_{N-1}^T \phi_{N-1}$ . By varying  $t$  different representation can be obtained, from the local ( $t \rightarrow 0$ ) to the global ( $t \rightarrow \infty$ ) structure of the network. Moreover, if  $D_k(u, v)$  is the number of paths of length  $k$  between nodes  $u$  and  $v$ , the following identity holds:

$$h_t(u, v) = e^{-t} \sum_{i=0}^{N^2-1} D_k(u, v) \frac{t^k}{k!} ,$$

which allows the explicit computation of the path length distribution:

$$D_k(u, v) = \sum_{i=0}^{N-1} (1 - \lambda_i)^k \phi_i(u) \phi_i(v) .$$

The proposed distance is just the Euclidean distance between the vectors of (ordered) eigenvalues (for a given matrix  $M$ ) for the two networks being compared:

$$(3) \quad d_M(G, H) = \sqrt{\sum_{i=0}^{N-1} \left( \lambda_i^{(G, M)} - \lambda_i^{(H, M)} \right)^2} ,$$

where  $\lambda_{(T, M)}$  are the eigenvalues of the graph  $T$  w.r.t. the matrix  $M$ , where  $M$  is either a connectivity matrix, or the heat kernel matrix or the path length matrix. As a final observation, the authors claim that the heat kernel matrix has the highest correlation with the edit distance, while the adjacency matrix has the lowest.

A similar formula D4 is proposed in [49] as the squared Euclidean ( $L_2$ ) between the vectors of the Laplacian matrix:

$$(4) \quad d(G, H) = \sum_{i=0}^{N-1} \left( \lambda_i^{(G, L)} - \lambda_i^{(H, L)} \right)^2 .$$

The next and last two measures are based on the concept of spectral distribution.

The distance D5 is introduced in [50], aiming at comparing Internet networks topologies. Let  $f_\lambda$  be the (normalized Laplacian) eigenvalued distribution, and  $\mu(\lambda)$  a weighting function and define a generic distance between graphs  $G$  and  $H$  as follows

$$d_{\mu, p}(G, H) = \int_{\lambda} \mu(\lambda) (f_{\lambda, G}(\lambda) - f_{\lambda, H}(\lambda))^p d\lambda .$$

The weighting function is then defined as  $\mu(\lambda) = (1 - \lambda)^4$ , an approximation of the graph irregularity as defined in [39], while the usual Euclidean metric is chosen, so that  $p = 2$ : the exact formula thus reads

$$(5) \quad d(G, H) = \int_{\lambda} (1 - \lambda)^4 (f_{\lambda, G}(\lambda) - f_{\lambda, H}(\lambda))^2 d\lambda .$$

Calculating the eigenvalues of a large (even sparse) matrix is computationally expensive; an approximated version is also proposed, based on estimation of the distribution  $f$  of eigenvalues by means of pivoting and Sylvester's Law of Inertia, used to compute the number of eigenvalues that fall in a given interval. To estimate the distribution  $K$  equally spaced bins in the range  $[0, 2]$  are used, so that a weighted spectral distribution measure for a graph  $G$  can be defined for an integer  $n > 0$  as follows:

$$\omega_n(G) = \sum_{k \in K} (1 - k)^n f(\lambda = k) .$$

The generic formula can be now specialized to:

$$(6) \quad d_n(G, H) = \sum_{k \in K} (1 - k)^n (f_G(\lambda = k) - f_H(\lambda = k))^2 ,$$

a family of metrics parameterized by the integer  $N$ .

The last spectral measure D6 in this review was presented in [51] and it employ two different divergence measures, Kullback-Leibler and Jensen-Shannon. The Kullback-Leibler divergence measure is defined on two probability distributions  $p_1, p_2$  of a discrete random variable  $X$  as

$$\text{KL}(p_1, p_2) = \sum_{x \in X} p_1(x) \log \frac{p_1(x)}{p_2(x)} .$$

The Kullback-Leibler divergence measure is not a metric, because is not symmetric and it does not satisfy the triangle inequality. To overcome this problem, the author consider the Jensen-Shannon measure, which in some sense is the symmetrization of KL:

$$\text{JS}(p_1, p_2) = \frac{1}{2} \text{KL} \left( p_1, \frac{p_1 + p_2}{2} \right) + \frac{1}{2} \text{KL} \left( p_2, \frac{p_1 + p_2}{2} \right) .$$

With this definition, the square root of JS is a metric. Thus, if  $f$  is the (normalized Laplacian) spectral probability distribution, a distance between two networks can be defined as

$$(7) \quad d(G, H) = \sqrt{\text{JS}(f_G, f_H)} .$$

Clearly, all the above distances D1-D6 suffer from the existence of isospectral graphs: they are relatively rare (especially in real networks) and qualitatively similar. For this reason, it would be more correct to call them distances between classes of isospectral networks. The six described distances are analytically summarized in Tab. 2.

We conclude mentioning that spectrum of the graph can be indirectly used for assessing similarity [52]. The authors employ a seriation method based on graph spectrum to convert the graph into a string so to get a sounder basis for the graph edit distance computation, aiming at the optimization of a function of the leading eigenvectors of the adjacency matrix.

### 3. BENCHMARKING EXPERIMENTS

In this section, we demonstrate the use of the distances in Tab. 2 in the comparison of network topologies in a controlled situation. To such aim, we constructed three synthetic benchmark datasets, detailed hereafter. All simulations have been performed within the R statistical environment [53]. Throughout all simulations, we kept, for each distance, the parameter values as in the reference paper wherever possible, e.g.,  $\gamma = 0.08$  for the scale of the Lorentz distribution in D2; the heat diffusion kernel in D3; the time  $t = 3.5$  for the kernel in distance D3. For D1 we choose to use the  $\lfloor \frac{N}{2} \rfloor$  largest eigenvalues.

TABLE 2. Spectral graph distances

Distance	Formula	Equation	Ref.
D1	$d_k(G, H) = \begin{cases} \sqrt{\frac{\sum_{i=N-k}^{N-1} (\lambda_i - \mu_i)^2}{\sum_{i=N-k}^{N-1} \lambda_i^2}} & \text{if } \sum_{i=N-k}^{N-1} \lambda_i^2 \leq \sum_{i=N-k}^{N-1} \mu_i^2 \\ \sqrt{\frac{\sum_{i=N-k}^{N-1} (\lambda_i - \mu_i)^2}{\sum_{i=N-k}^{N-1} \mu_i^2}} & \text{if } \sum_{i=N-k}^{N-1} \mu_i^2 < \sum_{i=N-k}^{N-1} \lambda_i^2 \end{cases}$	(1)	[46]
D2	$\epsilon(G, H) = \sqrt{\int_0^\infty [\rho_G(\omega) - \rho_H(\omega)]^2 d\omega}$	(2)	[47]
D3	$d_M(G, H) = \sqrt{\sum_{i=0}^{N-1} \left( \lambda_i^{(G,M)} - \lambda_i^{(H,M)} \right)^2}$	(3)	[48]
D4	$d(G, H) = \sum_{i=0}^{N-1} \left( \lambda_i^{(G,L)} - \lambda_i^{(H,L)} \right)^2$	(4)	[49]
D5e	$d(G, H) = \int_\lambda (1 - \lambda)^4 (f_{\lambda,G}(\lambda) - f_{\lambda,H}(\lambda))^2 d\lambda$	(5)	[50]
D5a	$d_n(G, H) = \sum_{k \in K} (1 - k)^n (f_G(\lambda = k) - f_H(\lambda = k))^2$	(6)	[50]
D6	$d(G, H) = \sqrt{\text{JS}(f_G, f_H)}$	(7)	[51]

**3.1. Data Description.** The simulated topologies are generated within the R statistical environment [53] by means of the simulator provided by the package *netsim* [54, 55], producing networks that reproduce principal characteristics of transcriptional regulatory networks. The simulator takes into account the scale-free distribution of the connectivity and constructs networks whose clustering coefficient is independent of the number of nodes in the network. All random graphs are generated by keeping the default values of *netsim* for the structural parameters.

In the first experiment we consider a random network  $A$  on  $N$  vertices and we compare it with the full connected network with the same number of nodes  $F$ , the complementary



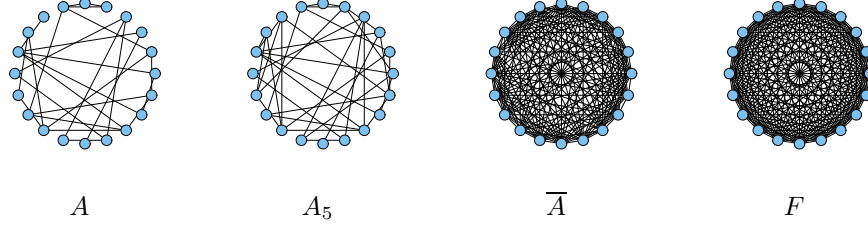


FIGURE 2. Benchmark Dataset  $\mathcal{B}_1(b, 25, 5)$ : the original graph  $A$ , the perturbed graph  $A_5$ , the complementary graph  $\bar{A}$  and the fully connected graph  $F$ .

network  $\bar{A}$  and a matrix  $A_p$  obtained from  $A$  by modifying (inserting/deleting) about the  $p\%$  of the nodes. For smoothing purposes, the process is repeated  $b$  times to obtain the first benchmarking dataset  $\mathcal{B}_1(b, N, p)$ . An instance of this benchmark dataset is shown in Fig.2. In Tab. 3 we show the average on  $b = 50$  instances of the number of nodes of the starting matrix  $A$  and the perturbed matrix  $A_5$ . Because of the small number of links in the original matrix, the 5% perturbation mostly reflects in links insertion. On average, the density of the original graph  $A$  can be expressed by the relation  $l \simeq 1.7N - 5$ , where  $l$  is the number of links and  $N$  the number of vertices.

In the second experiment we simulate a time-series of  $T$  networks on  $N$  nodes starting from a randomly generated graph  $S_1$ , where each successive element  $S_i$  of the series is generated from its ancestor  $S_{i-1}$  by randomly modifying  $p\%$  of the links. Again  $b = 50$  instances of the series are created and collected into the second benchmarking dataset  $\mathcal{B}_2(b, T, N, p)$ . With this strategy, the number of existing links is increasing with the series index, being the original adjacency matrix almost sparse. The starting matrix  $S_1$  has on average  $38.1 \pm 5.2$  nodes, while the last element of the series  $S_{20}$  has  $132.3 \pm 8.2$ . Three elements of this benchmark dataset are shown in Fig.3.

The third experiment is based on a benchmark dataset  $\mathcal{B}_3(b, T, N, nd, na)$ . Starting from  $\mathcal{B}_2(b, T, N, p)$ , different perturbations are applied: each successive element  $S_i$  of the series is generated from its ancestor  $S_{i-1}$  by randomly deleting  $nd$  links and adding  $na$  links. By construction, the number of existing links for all elements of the series is constant. Three elements of  $\mathcal{B}_3(b, 20, 25, 5, 5)$  are shown in Fig.4.

TABLE 3. Number of links in the original matrix  $A$ , in the fully connected matrix  $F$  (maximum number of links for the given dimension) and in the perturbed matrix  $A_5$ , expressed as mean  $\pm$  standard deviation on 50 replicates.

N	F	A	$A_5$
10	45	$13.4 \pm 2.0$	$13.1 \pm 2.3$
20	190	$29.0 \pm 3.6$	$36.6 \pm 5.2$
50	1225	$79.3 \pm 7.4$	$131.8 \pm 4.2$
100	4950	$164.5 \pm 13.6$	$388.2 \pm 12.1$

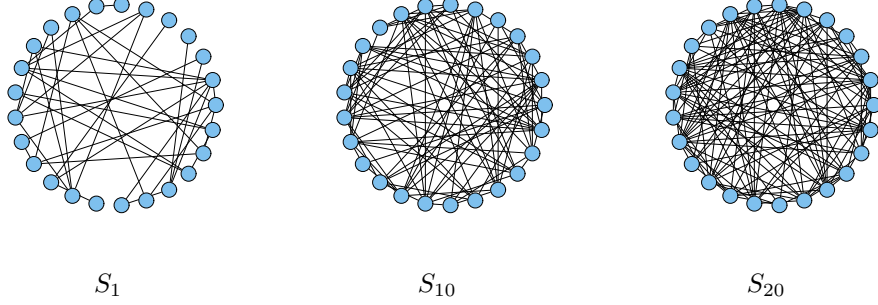


FIGURE 3. Benchmark Dataset  $\mathcal{B}_2(b, 20, 25, 5)$ : the original graph  $S_1$  (first element of the series), the tenth element  $S_{10}$  of the series and the final graph  $S_{20}$ .

**3.2. Results.** In Exp. 1 the six distances D1-D6 were applied on 4 instances of  $\mathcal{B}_1(50, N, 5)$  for  $N = 10, 20, 25, 100$  and distances between the original graph  $A$  and the three companion matrices  $F$ ,  $\bar{A}$  and  $A_p$  were computed. Results are collected in Tab. 4.

Distance D4 spans a considerably wider range than other measures, due to the absence of the square root in the comparison of the Laplacian spectra, while D5 is restricted into a very small interval. The same distance D4 also shows a high dependency on the dimension of the considered matrices and the number of the links (see Tab. 4).

The best stability in terms of the relative standard deviation  $\sigma/\mu$  is reached by D2 and D4. Furthermore, D2, differently from all other measures, is almost independent of the number of vertices. Finally, D6 is the only measure that, in the cases with  $N > 10$ , gives a lower distance for  $F$  than for  $\bar{A}$ .

The summary plots in Fig. 5 display results of Exp. 2 on the benchmark dataset  $\mathcal{B}_2(50, 20, 25, 5)$ . Distances between consecutive elements  $(S_i, S_{i+1})$  of the series (defined Step  $i$ ) were computed: results are averaged on the 50 replicates. For all D1-D6, distance decreases for increasing steps, although on different ranges (as already pointed out for Experiment 1) and with different widths for the confidence intervals. D3 and D5

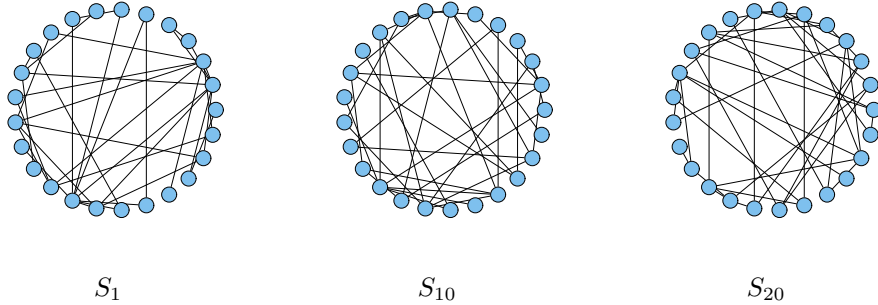


FIGURE 4. Benchmark Dataset  $\mathcal{B}_3(b, 20, 25, 5, 5)$ : the original graph  $S_1$  (first element of the series), the tenth element  $S_{10}$  of the series and the final graph  $S_{20}$ .

TABLE 4. Results of the experiments on the first benchmarking dataset. For each measure D1-D6 and number of network vertices  $N$ , the values are reported of the distances between the network  $A$  and the networks  $A_5$ ,  $\bar{A}$  and  $F$  in terms of the minimum (m), mean ( $\mu$ )  $\pm$  standard deviation and maximum (M) on the 50 replicates. Values of D5 are in  $10^{-3}$ .

N	D	$A_5$			$\bar{A}$			$F$		
		m	$\mu \pm \sigma$	M	m	$\mu \pm \sigma$	M	m	$\mu \pm \sigma$	M
10	1	0.025	0.108 $\pm$ 0.053	0.197	0.085	0.982 $\pm$ 0.383	1.564	0.424	1.324 $\pm$ 0.350	1.811
10	2	0.215	0.319 $\pm$ 0.052	0.403	0.47	0.857 $\pm$ 0.174	1.066	1.434	1.563 $\pm$ 0.04	1.635
10	3	0	0.067 $\pm$ 0.074	0.294	0.006	0.415 $\pm$ 0.39	1.83	0.028	0.472 $\pm$ 0.402	1.925
10	4	0	2.182 $\pm$ 1.01	4.533	14.33	151.8 $\pm$ 71.5	328.1	336	470.4 $\pm$ 61.7	598
10	5	0	0.941 $\pm$ 0.603	1.844	0.092	3.635 $\pm$ 2.340	8.907	0.518	4.112 $\pm$ 2.306	9.491
10	6	0.102	0.169 $\pm$ 0.039	0.259	0.192	0.386 $\pm$ 0.084	0.507	0.431	0.507 $\pm$ 0.04	0.552
20	1	0.037	0.194 $\pm$ 0.069	0.342	2.117	2.768 $\pm$ 0.379	3.71	2.455	3.038 $\pm$ 0.372	4.006
20	2	0.202	0.284 $\pm$ 0.049	0.381	1.025	1.091 $\pm$ 0.034	1.165	1.538	1.55 $\pm$ 0.008	1.568
20	3	0.044	0.154 $\pm$ 0.132	0.577	0.588	1.04 $\pm$ 0.333	2.05	0.643	1.103 $\pm$ 0.336	2.123
20	4	1.812	15.9 $\pm$ 6.5	28.5	2584	3658 $\pm$ 420	4761	4898	5531 $\pm$ 243	6146
20	5	0.358	0.836 $\pm$ 0.503	2.459	2.416	3.623 $\pm$ 6.441	1.041	2.439	3.654 $\pm$ 6.45	1.036
20	6	0.135	0.207 $\pm$ 0.04	0.323	0.581	0.772 $\pm$ 0.879	0.077	0.652	0.767 $\pm$ 0.83	0.05
50	1	0.389	0.504 $\pm$ 0.072	0.606	6.676	8.057 $\pm$ 0.784	9.064	6.924	8.288 $\pm$ 0.771	9.253
50	2	0.275	0.344 $\pm$ 0.042	0.437	1.152	1.195 $\pm$ 0.025	1.228	1.533	1.54 $\pm$ 0.005	1.549
50	3	0.668	1.186 $\pm$ 0.313	1.77	2.078	3.356 $\pm$ 0.647	4.428	2.138	3.423 $\pm$ 0.649	4.497
50	4	138	237 $\pm$ 48	353	83850	92670 $\pm$ 3078	97710	102700	107300 $\pm$ 1613	110000
50	5	0.888	1.875 $\pm$ 0.541	2.765	2.379	3.993 $\pm$ 0.847	5.42	2.379	3.992 $\pm$ 0.849	5.42
50	6	0.435	0.559 $\pm$ 0.0751	0.711	1.372	1.481 $\pm$ 0.061	1.597	1.183	1.277 $\pm$ 0.063	1.39
100	1	0.804	0.977 $\pm$ 0.076	1.086	13.55	16.07 $\pm$ 1.032	17.6	13.77	16.28 $\pm$ 1.027	17.8
100	2	0.451	0.506 $\pm$ 0.025	0.544	1.215	1.264 $\pm$ 0.019	1.293	1.524	1.533 $\pm$ 0.004	1.543
100	3	2.116	3.606 $\pm$ 0.665	4.64	4.506	6.723 $\pm$ 0.992	8.166	4.566	6.79 $\pm$ 0.995	8.238
100	4	1784	2161 $\pm$ 136	240	842900	861200 $\pm$ 9575	880600	915800	925100 $\pm$ 4880	935900
100	5	1.645	2.787 $\pm$ 0.525	3.589	2.602	3.941 $\pm$ 0.630	4.824	2.602	3.941 $\pm$ 0.631	4.824
100	6	0.933	1.102 $\pm$ 0.074	1.204	2.07	2.229 $\pm$ 0.088	2.397	1.694	1.839 $\pm$ 0.078	1.997

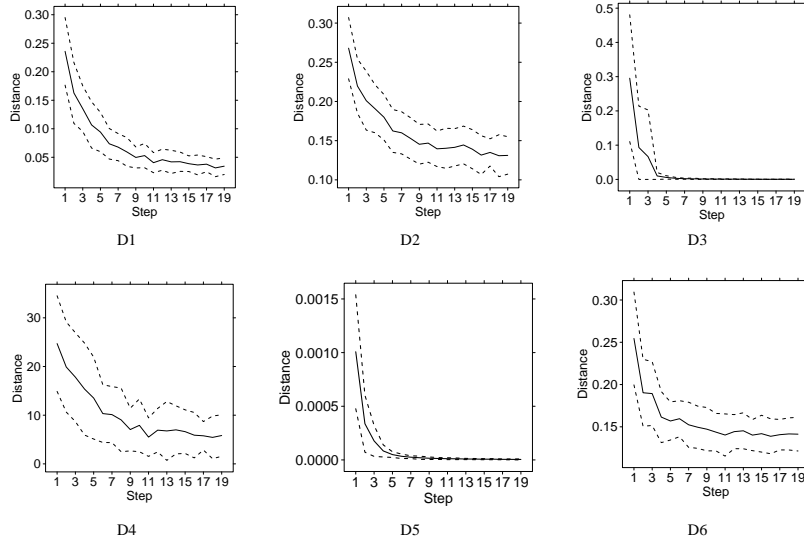


FIGURE 5. Plots of the distances of consecutive elements of the series of the dataset  $B_2(50, 20, 25, 5)$ . Solid line: mean over the  $b = 50$  replicates; dashed lines:  $1\sigma$  standard deviation confidence intervals.

decrease more quickly for initial steps, so they are less useful when comparing large networks.

To better highlight similarities and differences among the distances regardless of their ranges of values, we also computed their mutual correlations and plotted the mutual scatter plots in Fig. 6. All correlation values are quite high, ranging from 0.8225 to 0.9970: D3 and D5 are mutually strongly correlated, but they tend to separate from the other distances, as evidenced both from the global correlation values and the scatter plot profiles distancing from the panel diagonals.

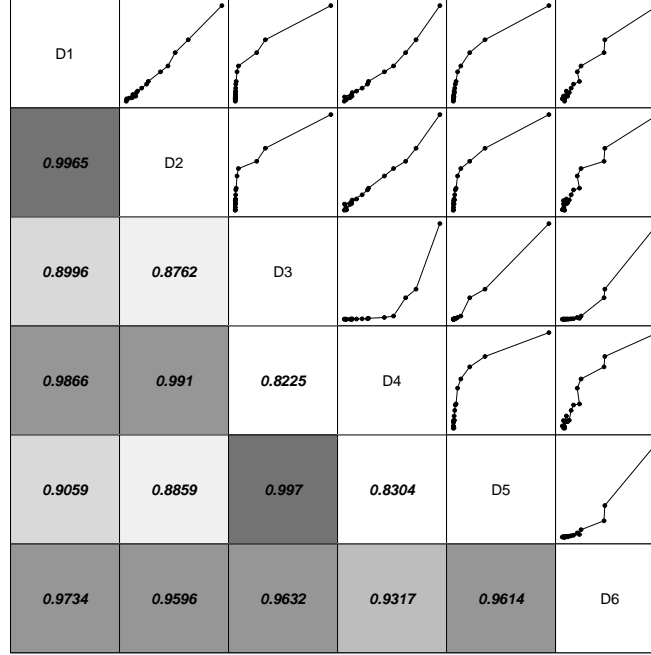


FIGURE 6. Mutual scatterplots (upper triangle) and correlation values (lower triangle) for the Exp. 2.

The Experiment 3 was performed on the benchmark dataset  $\mathcal{B}_3(50, 20, 25, 5, 5)$ , and the results are reported in two figures matching those of Exp. 2. Since the difference between consecutive pairs of elements of the series is quite similar throughout all the steps, as expected all distances show a nearly constant trend as shown in Fig. 7.

The oscillations around the mean value are nevertheless strongly varying among different measures, as evidenced by Fig. 8. In particular, distance D3 is anticorrelated to all distances but D5; furthermore only in 4 cases out of 15 we obtain a correlation value higher than 0.7, with again D1, D2, D4 and D6 forming a group of more similar behaviour.

Possible hierarchy of the six distances was explored by clustering. Two dendrograms are built for Exp. 2 and Exp. 3 by using the *hclust* package in R and shown in Fig. 9. The clusters have average linkage and the correlation distance  $cd(\cdot, \cdot) = 1 - \text{Corr}(\cdot, \cdot)$  is used as the dissimilarity measure. Although there is an appreciable coherence among measures on macroscopic trends, when downscaling to microscopic trends correlations get much looser. Distances D1, D2, D4, D6 seem to group together, while D3 has a more erratic behaviour. Finally, a wide range difference occurs in the cluster heights between the

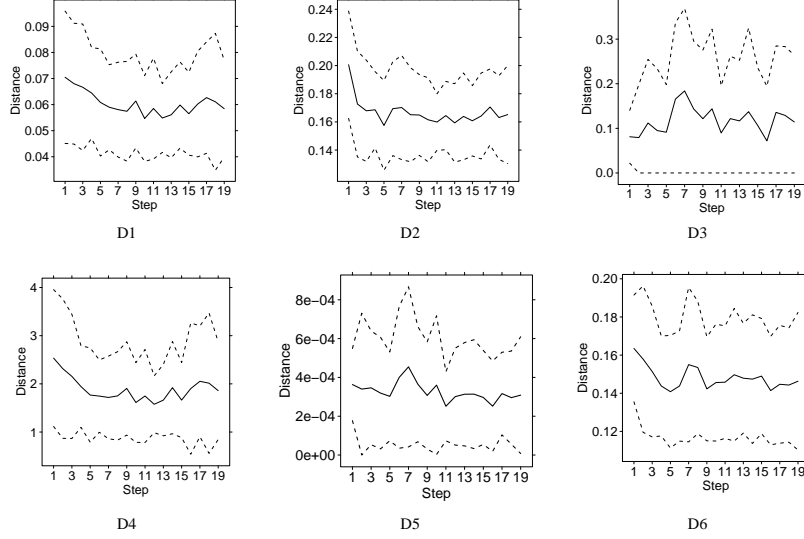


FIGURE 7. Plots of the distances of consecutive elements of the series of the dataset  $\mathcal{B}_3(50, 20, 25, 5, 5)$ . Solid line: mean over the  $b = 50$  replicates; dashed lines:  $1\sigma$  standard deviation confidence intervals.

two experiments: the homogeneous macroscopic situation of Exp. 2 has a narrower height span than the microscopic case in Exp. 3.

#### 4. A REGULATORY NETWORK EXAMPLE

To conclude with, we apply D1-D6 to three different perturbations of the transcriptional interactions network<sup>3</sup> in *Escherichia coli*, described in [56] and shown in Fig. 10.

The transcriptional database contains 577 interactions between 116 TFs and 419 operons. Starting from an existing database (RegulonDB<sup>4</sup>), the authors added 35 new TFs, including alternative sigma factors, and over a hundred new interactions from the literature. The original adjacency network (without self-interactions) consists of 420 vertices and 519 (undirected) links. To show the influence on distances, we compare the distances between the original network and the three networks obtained by silencing out (thus deleting the link involving such vertex) the activator/repressor factor *crp* and the two repressor factors *frn* and *himA*, having respectively 72, 22 and 21 links. In Tab. 5 we list the value of the distances between the original network  $EC$  and its three perturbations, denoted respectively as  $EC_{\overline{crp}}$ ,  $EC_{\overline{frn}}$  and  $EC_{\overline{himA}}$ .

All distances seem to be heavily dependent on the number of removed links: for all six distances,

$$D(EC, EC_{\overline{crp}}) > D(EC, EC_{\overline{frn}}), D(EC, EC_{\overline{himA}}).$$

Nevertheless, when the number of removed links are almost equal, such relation is not valid anymore.

<sup>3</sup>Publicly available at [http://www.weizmann.ac.il/mcb/UriAlon/Network\\_motifs\\_in\\_coli/ColiNet-1.1/](http://www.weizmann.ac.il/mcb/UriAlon/Network_motifs_in_coli/ColiNet-1.1/)

<sup>4</sup><http://regulondb.ccg.unam.mx/>

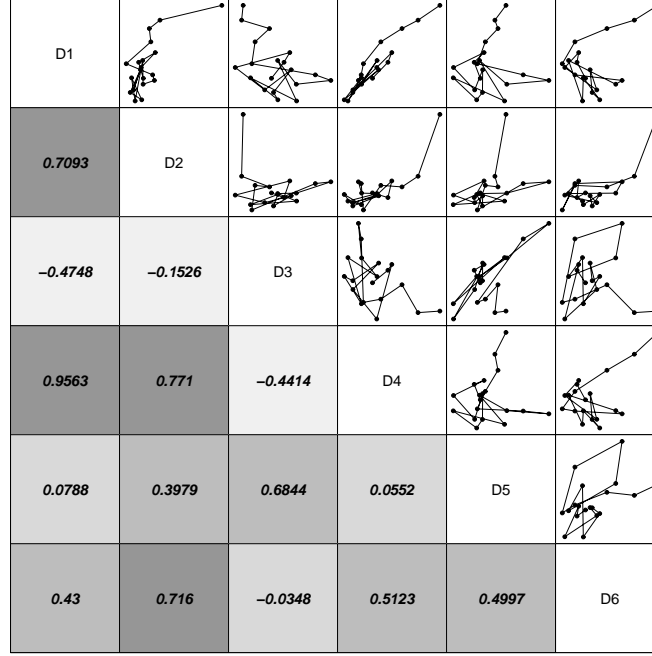


FIGURE 8. Mutual scatterplots (upper triangle) and correlation values (lower triangle) for the Exp. 3.

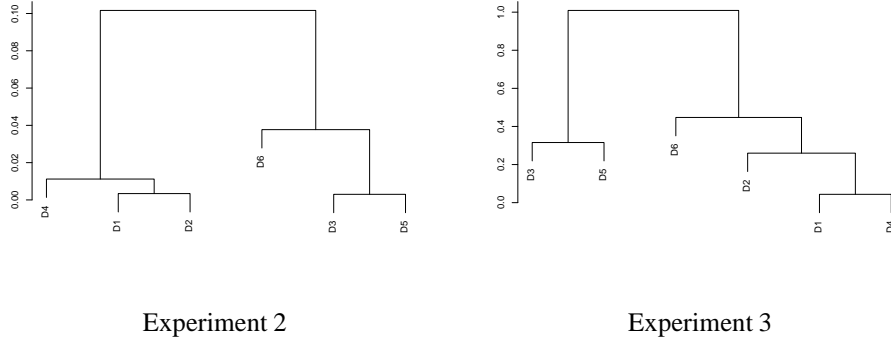


FIGURE 9. Cluster dendrograms with average linkage and correlation distance of D1-D6 for the two Experiments 2 and 3.

The distance  $D(EC, EC_{\overline{himA}})$  is comparable to  $D(EC, EC_{\overline{fnr}})$  for  $D = D1, D4$ , while the former is much bigger than the latter for all other distances. In fact,

$$\frac{D(EC, EC_{\overline{himA}})}{D(EC, EC_{\overline{fnr}})} \simeq \begin{cases} 2.8 & \text{for D2} \\ 4.8 & \text{for D6} \\ 27 & \text{for D3} \\ 35 & \text{for D5} \end{cases}$$

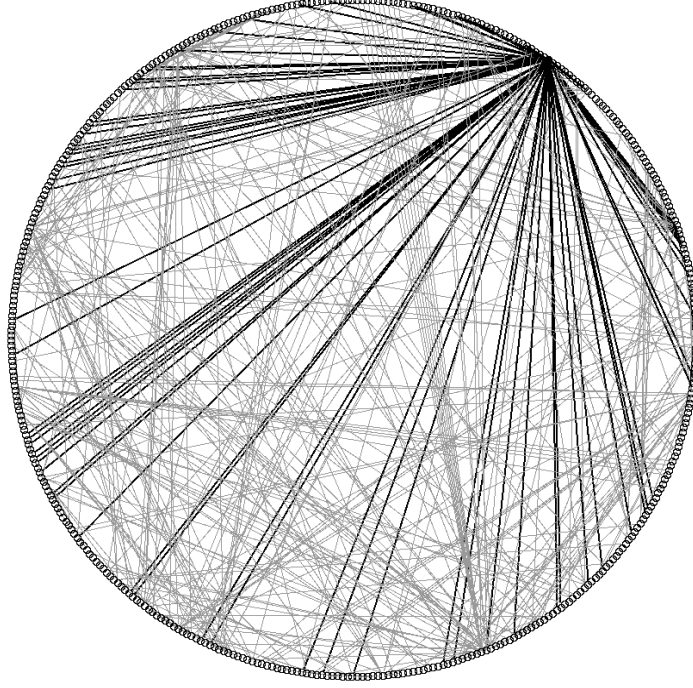


FIGURE 10. Transcriptional interactions network for *Escherichia coli*, with edges relative to gene *crp* marked in black.

TABLE 5. Distances between  $EC$  and the perturbed networks  $EC_{\overline{crp}}$ ,  $EC_{\overline{fnr}}$  and  $EC_{\overline{himA}}$ .

Network	Links	D1	D2	D3	D4	D5	D6
$(EC, EC_{\overline{crp}})$	519 vs 453	0.418	0.085	8.711	2191.9	$1.01178 \cdot 10^{-3}$	0.555
$(EC, EC_{\overline{fnr}})$	519 vs 497	0.058	0.023	0.191	41.4	$0.01256 \cdot 10^{-3}$	0.083
$(EC, EC_{\overline{himA}})$	519 vs 498	0.056	0.065	5.187	44.4	$0.43315 \cdot 10^{-3}$	0.404
$(EC_{\overline{crp}}, EC_{\overline{fnr}})$	453 vs 497	0.557	0.074	6.938	2140.9	$0.82079 \cdot 10^{-3}$	0.479
$(EC_{\overline{crp}}, EC_{\overline{himA}})$	453 vs 498	0.557	0.072	0.982	2138.1	$0.26794 \cdot 10^{-3}$	0.180
$(EC_{\overline{fnr}}, EC_{\overline{himA}})$	497 vs 498	0.023	0.071	3.730	10.2	$0.30303 \cdot 10^{-3}$	0.357

For instance, the corresponding ratios  $D(EC, EC_{\overline{crp}})/D(EC, EC_{\overline{himA}})$  are much smaller, namely

$$\frac{D6(EC, EC_{\overline{crp}})}{D6(EC, EC_{\overline{himA}})} \simeq 1.4 \quad \text{and} \quad \frac{D3(EC, EC_{\overline{crp}})}{D3(EC, EC_{\overline{himA}})} \simeq 1.7 .$$

TABLE 6. Natural logarithm of the size of the automorphism group of the original and the perturbed networks

Network $\mathbf{G}$	$\log( \text{Aut}(\mathbf{G}) )$	$\max\{\lambda_i\}$
$EC$	330.0173	73.021
$EC_{\overline{crp}}$	377.5827	27.015
$EC_{\overline{fnr}}$	341.4692	73.019
$EC_{\overline{himA}}$	347.4488	73.020

A possible explanation is in the quite different structure of the two networks  $EC_{\overline{fnr}}$  and  $EC_{\overline{himA}}$ , although being obtained silencing out almost the same number of links from the original network.

The intrinsic structural difference between  $EC_{\overline{fnr}}$  and  $EC_{\overline{himA}}$  is indeed highlighted by the remarkable variation in the size of the respective group of automorphisms as shown in Tab. 6. For instance, the structure of  $EC_{\overline{himA}}$  is almost  $e^{347.4488-341.4692} \simeq 400$  times more symmetric than  $EC_{\overline{fnr}}$ . From this point of view, spectral distances can greatly help in analyzing subtle differences between networks where more classical methods are not helping much. As an example, the leading Laplacian eigenvalue is commonly used when network structure, because it is a good indicator of the stability and the local dynamics [57]. For instance, in this particular example, this value is of no help, as indicated in Tab. 6, since  $EC$ ,  $EC_{\overline{fnr}}$  and  $EC_{\overline{himA}}$  have essentially the same leading eigenvalue; nevertheless the spectral distances, encoding information coming from the whole spectrum, can better separate very similar networks. Summarizing the observations following the experiments on synthetic data and the results in Tab. 5, we can conclude proposing  $D2$  as the more reliable metric, both in terms of stability and robustness in terms of being less prone to odd behaviours.

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